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***************************************		我的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的,我们就是我们的我们的我们的,我们就是我们的,我们是我们的,我们是我们的,我们们的我们的,
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Wed Aug 16 09:45:30 2000; MasPar time 13.16 Seconds 531.967 Million cell updates/sec MPsrch_pp

Tabular output not generated.

Title:

>US-09-427-873-2 (1-101) from US09427873.pep 683 1 LGKFSQTCYNSAIQGSVLTS.....STKINLDDHIANIDGTLKYE 101 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 segs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 38.316; Variance 63.692; scale 0.602 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	9	% Query	% Query Match Tenath DB	9	f		i di
2	3007	וומ רכוו	יייי פיייי	9 :	11	Desci ipcion	FIEG. NO.
н	107	15.7	325	10	939705	1-AMINOCYCLOPROPANE-1-	2.18e-04
7	100	14.6	168	~	031938	YONX PROTEIN.	3.43e-03
m	100	14.6	168	σ	064083	HYPOTHETICAL 19.6 KD P	3.43e-03
4	96	14.1	271	10	038960	1-AMINOCYCLOPROPANE-1-	1.58e-02
S	93	13.6	999	7	P72529	PENICILLIN-BINDING PRO	4.86e-02
9	92	13.5	318	10	092021	1-AMINOCYCLOPROPANE-1-	7.03e-02
7	91	13.3	282	20	064945	ACC OXIDASE 1.	1.02e-01
۵	91	13.3	314	10	082127	ACC OXIDASE.	1.02e-01
σ	91	13.3	417	4	906660	DIIIC (RHD) (FRAGMENT)	1.02e-01
10	90	13.2	999	~	P72528	PENICILLIN-BINDING PRO	1.46e-01
11	90	13.2	667	4	043313	KIAA0431.	1.46e-01
12	88	13.0	317	10	041681	1-AMINOCYCLOPROPANE-1-	2.10e-01
13	89	13.0	481	7	P76052	FROM BASES 1389923 TO	2.10e-01
14	88	12.9	202	Н	051967	ORF H0211.	3.01e-01
15	88	12.9	999	7	054474	PENICILIN-BINDING PROT	3.01e-01
16	88	12.9	999	7	033681	PBP2X (FRAGMENT).	3.01e-01
17	87	12.7	999	~	P95804	PENICILIN-BINDING PROT	4.30e-01
18	98	12.6	544	Н	Q9YEG2	544AA LONG HYPOTHETICA	6.13e - 01
19	85	12.4	318	10	043613	1-AMINOCYCLOPROPANE-1-	8.71e-01
20	82	12.4	407	9	097958	RH30-LIKE PROTEIN (FRA	8.71e-01

130 LLDL 133

qq

1.24e+00	1.24e+00	1.75e+00	1.75e+00	1.75e+00	1.75e+00	1.75e+00	1.75e+00	1.75e+00	1.75e+00	1.75e+00	7.	2.46e+00	2.46e+00	2.46e+00	2.46e+00	3.46e+00	3.46e+00	3.46e+00	3.46e+00	3.46e+00	4.84e+00	4.84e+00	4.84e+00	4.84e+00
F31D4.8 PROTEIN.	PENICILLIN-BINDING PRO	CORONATINE-INDUCED PRO	UNKNOWN.	ANTHRANILATE SYNTHASE	FOIG10.1 PROTEIN.	PBP2X (FRAGMENT).	PBP2X (FRAGMENT).	PENICILLIN-BINDING PRO	GAMMA-TUBULIN RING PRO	COXI INTRON1 ORF.	HYPOTHETICAL PROTEIN.	HISTIDINE KINASE SENSO	ACC OXIDASE 2.	DEF PROTEIN (CLA1).	TRANSKETOLASE (FRAGMEN	COSMID F56C9.	SA COMPONENT.	SIMILARITY TO A GROUND	PENICILLIN BINDING PRO	POLYPROTEIN PP220.	HYPOTHETICAL PROTEIN.	HISTIDINE KINASE SENSO	GDP-D-MANNOSE-4,6-DEHY	PBP2X (FRAGMENT).
045423	070035	022527	068560	028668	017759	033660	033692	P72531	O9XYP7	Q35063	022257	031141	064946	023407	049738	020865	006497	001465	054781	008358	038500	031140	075357	033676
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180	9		475	546	618	999	999	999	819	902	173	252	318	717	739	237	460	518	999	2475	31	253	339	999
.12.3	12.3	12.2	12.2	12.2	12.2	12.2		12.2	12.2	12.2	12.0	12.0	12.0	12.0	12.0	11.9	11.9	11.9	11.9	11.9	11.7	11.7	11.7	11.7
84	84		ё 8	83	83		83	83					82	82	82	81	81	81	81	81	80	80	80	80
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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5; Gaps

Length 168

LT 2 031938 031938;

RESULT

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41 ASKGLEAVQNQIDD-LDWESTFYIRHLPESNISEIPDLEDEYRKVMREFAKELEKLAENI 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| |::| ::| ::| ::| ::| 32 SSIDLNSVIENVDGSLKWQPSNFIETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helianthus annuus (Common sunflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Asteridae; eussterids II; Asterales; Asteraceae;

Asteroideae; Helianthus.
                                                                                                                                                                                               Bacteriophage SPBC2.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
KARAKEVIC V., DUESTERHOEFT A., SOLDO B., HILBERT H., MAUEL C.,
KARAKATA D.;
KARAKATA D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              039960;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB 9; Length 168
Pred. No. 3.43e-03;
29; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96; DB 10; Length 271
Pred. No. 1.58e-02;
22; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC120713; ARC13043.1; -.
Hypothetical protein
SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;
                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
HYPOTHETICAL 19.6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 AA; 31079 MW; 01B8149C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666 AA.
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Best Local Similarity 24.1%;
watches 21; Conservative
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Local Similarity 20.6%;
les 13; Conservative
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SEQUENCE
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ID P72529
AC P72529;
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Q39960
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RAY MEDLINE; 98044031

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RAY BENELINE; C. BRANS A., BRAUN A., BORCHERT S., BORCHERT S., BARESTER L. S.C., BRON S., BROUTLET S., BRUSCHI C. V., CALDWELL B., CAPUANO V., CARTER N.A., BROUTLET S., BRUSCHI C. V., CALDWELL B., CAPUANO V., CARTER N.A., CHOIS.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANNEL R.A., BRUSCHIE K.A., EARLICHS S.D., EMMESON P.T., RAY ENTION K.D., ERRINGTON J., FABRET C., FULLICH S.D., CARLERON N., CHILLERY H., HOLSAPPEL S., HOSONO S., HOLLOM K.D., GRALLERON N., ALIEBRY H., HOLSAPPEL S., HOSONO S., HOLLOM M.F., ITAYA M., JONES L., ACONTER P., COFFEAU S., KORONO S., HORLOW M., KLEIN C., ACONTER P., LEVINE A., LANDINOIS S., LAUBER JANGARI S., KUMANO M., ACORTER P., LOFFEAU S., SOLOS S., KUMANO M., MELLADO R.P., MIZUNO M., WOESTL D., NAKAI S., NODBACK M., RANDINA R., LEVINE A., LOTHIN M., PORTETELLE D., PORMOLLIK S., PRESCOTT A.M., PORTETELLE D., PORMOLLIK S., PRESCOTT A.M., RENNOLDS S., RAPOPORT G., REY M., REVOLTS C., PUTIC P., PURNELLE B., ROCHE B., ROSE M., SADAIE Y., ACONIA S., SERON S., SCHROETER R., SANDAIE Y., ACONIA S., SERON S., SCHROETER R., SANDAIE Y., ACONIA S., SERON S., SHIN B.S., SOLDO B., SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., STIN B.S., SOLDO B., SEKIGUCHI J., TARARASHI H., TARKEMARU K., TARCONI E., TARARASHI H., TARKEMARU K., TARCONI E., TARARASHI H., TARKENARU K., TARKENARU H., TARKENARU K., TARCONI E., WEDLER H., WEITZENEGGER T., WEDLER H., WEITZENEGGER T., WEDLER H., WEITZENEGGER T., WEDLER H., WEITZENEGGER T., TARKENES P., WIDMA A., YANDENE E., WEDLER H., WEITZENEGGER T., WEDLER H., WEITZENEGGER T., TARKEN H., WEDLER H., WEITZENEGGER T., TARKEN H., TARKENARU H., YANDENE E., WEDLER H., WELLER H., WELL
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Pred. No. 3.43e-03;
29; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299115; CAB14015.1; -.
SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;
                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                168 AA.
                                                                                                                                                                                                                             Created)
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                                                                                                                                                                PRT;
                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.1%;
Matches 21; Conservative
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98044033.
                                                                                                                                                                                                                                                                                                                             YONY PROTEIN
                           94
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91 IANI
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168 AA

PRT;

PRELIMINARY;

RESULT 3 ID 064083

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Length 271;

Tracheophyta;

M.A.J.;

S., PARRY

Gaps

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67 HIASKGLNDVVTEVND-VDWESTFFLRHLPVSNIADLPELSDDYKSVMKQFASKLQVLAE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumis sativus (Cucumber).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHIOMI S., YAMAMOTO M., ONO T., KAKIUCHI K., NAKAMOTO J.,
NAKATSUKA A., KUBO Y., NAKAMURA R., INABA A., IMASEKI H.;
"CDNA cloning of ACC synthase and ACC oxidase genes in cucumber and their differential expression by wounding and auxin.";
J. Jpn. Soc. Hort. Sci. 67:685-692(1998).
EMBL; AB006807; BAA33378.1;
MENDEL; 32730; Cucsa; Aco; 32730.
   Cucumis sativus (Cucumber).

Bukaryotis, Uridiplantae; Streptophyta; Embryophyta; Tracheophyt.

Bukaryota; Viridiplantae; Streptophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; orre eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.3%; Score 91; DB 10; Length 282; Best Local Similarity 25.0%; Pred. No. 1.02e-01; Matches. 15; Conservative 17; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                               SEQUENCE FACE. .....
TISSUE-FLORAL BUDS;
PERL-TREVES R., KAHANA A., KORACH T., KESSLER N.;
PREL-TREVES R., KAHANA A., KORACH T., KESSLER N.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF033581; AAC67232.1; -..
MENDEL; 28786; CLOSS3,800.28786.
PFAM; PF00671; Fe_ASC_OXIGOTEd; 1.
SEATH, PEORG A.; 31795 MW; 9C7C682F CRC32;
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Last annotation update)
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Last annotation update)
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TISSUB-FLORAL BUDS.
TYAN J.E., ANDRALOJC P.J., WILLIS A.C., GUTTERIDGE
Plant Physiol. 116:1192-1192(1998).
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SEQUENCE 314 AA; 35470 MW; 640C59E4 CRC32;
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12,
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01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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01-NOV-1998
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Q99906;
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TISSUE-FLOWER ORGAN;
TASSUE-FLOWER ORGAN;
TASSUE-FLOWER C.J.;
TASSUE-FLOWER C.G.S.;
TASSUE-FLOWER C.G. GOH C.J.;
TASSUELION OF A CDNA Clone Encoding 1-Aminocyclopropane-1-Carboxylate Oxidase from Dendrobium crumenatum (Accession No. AF038840) (PGR99-015).;
Plant Physiol. 119:805-805(1999).
Plant Physiol. 119:805-805(1999).
EMBL, AF038840; AAD02104.1; -.
MENDEL; 35903; Dencu; Aco; 35903.
SEQUENCE 318 AA; 36132 MW; 16E0E31C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 DASVEGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGS-KSLLGTFGLESSLNTILAGT 146
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                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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9
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Pred. No. 7.03e-02;
20; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                      REICHMAN P., KOENIG A., MARTON A., HAKENBECK R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X98356; XA67012.1, Tanspeptidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NAY-1999 (TrEMBLrel. 10, Created)
01-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PENICILLIN-BINDING PROTEIN (FRACMENT)
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Last annotation update)
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Pred. No. 4.86e-02;
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Local Similarity 23.3%;
hes 14; Conservative
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t Local Similarity 29.8%;
ches 28; Conservative
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01-AUG-1998 (TrEMBLrel. 0°
01-NOV-1999 (TrEMBLrel. 1.)
ACC OXIDASE 1.
CS-ACO1.
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666 AA;
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                                                                                                            Homo sapiens (Human).
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                             01-JUN-1998 (
01-JUN-1998 (
01-MAY-1999 (
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Q41681;
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                                                                        BECKERS E.A., FAAS B.H., LIGTHART P., SIMSEK S., OVERBEEKE M.A., DEM BORNE A.E., VAN RHENEN D.J., DER SCHOOT C.E.; Characterization of the hybrid RHD gene leading to the partial D category IIIc phenotype."; Transfusion 36:567-574(1996).
                                                                                                                                                                                                                    "Alteration of RH gene structure and expression in human dCCee DCW-red blood cells: phenotypic homozygosity versus genotypic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                               Score 91; DB 4; Length 417; Pred. No. 1.02e-01; 31; Mismatches 36; Indels
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Pred. No. 1.46e-01;
23; Mismatches 37; Indels
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REICHMAN P., KOENIG A., MARTON A., HAKENBECK R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBU databases.
EMBL; X98365; CAA67011.1;
PFAM; PF00905; Transpeptidase; 1.
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                                                                                                                                                                                                                                                  heterozygosity.";
Blood 88:2326-2333(1996).
EMBL; S82449; AAB37696.1;
ABL; S83379; CAB34097.1;
FAM; PF00909; Ammonium_transp; 1.
NON_TER 417 AA; 45099 MW; BCB0B58F CRC32;
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72761 MW; OBFBAD9A CRC32;
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Local Similarity 29.8%;
les 28; Conservative
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13.3%;
Best Local Similarity 22.6%;
Matches
21; Conservative
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HUANG C.H.;
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Phaseolus aureus (Mung bean) (Vigna radiata).
Bukaryota; Viridiplantues, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                                                                                                                                                                                  ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N., OHARA O.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; BARD7891; BAA48611; -
PFRM; PF00096; zf-C2Hz; 2.
SEQUENCE 667 AA; 72334 MW; 19900DE91CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 LESVQSEIND-LDWESTFFLRHLPVSNVSENTDLDQDYRKIMKQFAEELEKLAEHLLDL 131
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"Structure and expression of cDNAs encoding 1-aminocyclopropane-1-carboxylate oxidase homologs isolated from excised mung bean hypocoryls.";

Planta 194:223-2291994).

EMBL, UGGOAG, AACAG921.1; -.

MENDEL, 504; Phaau, Aco;504.

PRAM; PF00671; Fe_Asc_Oxidored; 1.

SEQUENCE 317 AA; 35773 MW; F02E6272 CRC32;
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last sequence update)
Last annotation update)
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Best Local Similarity 22.9%; Pred. No. 1.46e-01;
Matches 16; Conservative 21; Mismatches 31
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SEQUENCE 1
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BLATTNER F.R., PLUNKETI III G., BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASKER J.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.,
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JONES J.G., YOUNG D.C., DASSARWA S.;

Structure and organization of the gas vesicle gene cluster on the Halobacterium halobium plasmid pNRC100.";
Gene 102:117-122(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJNE; 90016863.
JONES J.G., HACKETT N.R., HALLADAY J.T., SCOTHORN D.J., YANG C.F.,
NG W.L., DASSARMA S.;
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
FROM BASES 1389923 TO 1402712
(SECTION 121 OF THE COMPLETE GENOME (SECTION 121 OF 400)
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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MEDLINE; 91267967.
MEDLINE; 91267967.
MG W.L., KOTHAKOTA S., DASSARWA S.;
"Structure of the gas vesicle plasmid in Halobacterium halobium inversion isomers, inverted repeats, and insertion sequences.";
J. Bacteriol. 173:3933-3933(1991).
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DASSARMA S., DAMERVAL T., JONES J.G., TANDEAU DE MARSAC N.;
"A plasmid-encoded gas vesicle protein gene in a halophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
EMBL; ASC74119.11; ... SEQUENCE 481 AA; 52193 MW; 8C5C0196 CRC32;
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Best Local Similarity 30.0%; Pred. No. 2.10e-01;
Matches 12; Conservative 12; Mismatches 16; Indels
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01-MAY-1999 (TrEMBLrel.
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Plasmid pNRC100.
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Winimal replication origin of the 200-kilobase Halobacterium plasmid
pMRC100.",
                                                                                                                                                                                                                                                                                                                MEDLINE; 93139036.

HALLADAY J.T., JONES J.G., LIN F., MACDONALD A.B., DASSARMA S.;

"The rightward gas vesicle operon in Halobacterium plasmid pNRC100:
identification of the gvpA and gvpC gene products by use of antibody
probes and genetic analysis of the region downstream of gvpC.";
J. Bacteriol. 175:684-692(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95095934.

DASSARMA S., ARORA P., LIN F., MOLINARI E., YIN L.R.;
"Wild-type gas vesicle formation requires at least ten genes in the gyp gene cluster of Halobacterium halobium plasmid pNRC100.";
J. Bacteriol. 176:7646-7652(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NG W.L., CIUFO S:A., SMITH T.M., BUMGARNER R.E., LORETZ C., BASKIN FAUST J., SETO J., SLAGEL J., HOOD L., DASSARMA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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NG W.L., CIUFO S.A., SMITH T.M., BUMGARNER R.E., LORETZ C., BASKIN
NG W.L., CIUFO J., SLAGEL J., HOOD L., DASSARMA S.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016485; AAC82797.1; -.
                                                                                       HALLADAY J.T., NG W.L., DASSARWA S.; "Genetic transformation of a halophilic archaebacterium with a gas vesicle gene cluster restores its ability to float.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DASSARMA S.;
"Identification and analysis of the gas vesicle gene cluster on
unstable plasmid of Halobacterium halobium.";
Experientia 49:482-486(1993).
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Cold Spring Harbor Laboratory Press, New York (1995)
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NG W.L., ARORA P., DASSARMA S.;
Syst. Appl. Microbiol. 16:560-568(1994).
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FEMS Microbiol. Lett. 153:1-10(1997).
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MEDLINE; 93327890.
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MEDLINE; 93328662.
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                           STRAIN-NRC-1;
MEDLINE; 93012964
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STRAIN-10712;
STRAIN-10712;
MEDLINE, 95020605.
SIBOLD C., HENRICHSEN J., KOENIG A., MARTIN C., CHALKLEY L.,
HAKENBECK R.;
"MOSAIC pbpX genes of major clones of penicillin-resistant
Streptococcus pneumoniae have evolved from pbpX genes of a penicillin-
sensitive Streptococcus oralis.";
Mol. Microbiol. 12:1013-1023(1994).
EMBL, X78216; CAA55061.1;
PFAM; PF00905; Transpetidase; 1.
NON_TER
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Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
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Pred. No. 3.01e-01;
26; Mismatches 36; Indels
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666 AA; 72906 MW; FD424A39 CRC32;
                                 202 AA; 23627 MW; 2DEF3572 CRC32;
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Best Local Similarity 25.6%;
Matches 22; Conservative
PFAM: PF00096; zf-C2H2; 1. Plasmid. SEQUENCE 202 AA; 23627
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